

M. Mosher

1643

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**RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/879,827A**

DATE: 01/27/1999  
TIME: 15:55:05

**INPUT SET: S30367.raw**

**This Raw Listing contains the General Information Section and up to the first 5 pages.**

**SEQUENCE LISTING**

3 (1) General Information:  
4  
5 (i) APPLICANT: Jofuku, K. Diane  
6 Okamuro, Jack K.  
7  
8 (ii) TITLE OF INVENTION: Methods for Improving Seeds  
9  
10 (iii) NUMBER OF SEQUENCES: 111  
11  
12 (iv) CORRESPONDENCE ADDRESS:  
13 (A) ADDRESSEE: Townsend and Townsend and Crew LLP  
14 (B) STREET: Two Embarcadero Center, Eighth Floor  
15 (C) CITY: San Francisco  
16 (D) STATE: California  
17 (E) COUNTRY: USA  
18 (F) ZIP: 94111-3834  
19  
20 (v) COMPUTER READABLE FORM:  
21 (A) MEDIUM TYPE: Floppy disk  
22 (B) COMPUTER: IBM PC compatible  
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
25  
26 (vi) CURRENT APPLICATION DATA:  
27 (A) APPLICATION NUMBER: US 08/879,827  
28 (B) FILING DATE: 20-JUN-1997  
29 (C) CLASSIFICATION:  
30  
31 (vii) PRIOR APPLICATION DATA:  
32 (A) APPLICATION NUMBER: US 08/700,152  
33 (B) FILING DATE: 20-AUG-1996  
34  
35 (viii) ATTORNEY/AGENT INFORMATION:  
36 (A) NAME: Bastian, Kevin L.  
37 (B) REGISTRATION NUMBER: 34,774  
38 (C) REFERENCE/DOCKET NUMBER: 023070-067210US  
39  
40 (ix) TELECOMMUNICATION INFORMATION:  
41 (A) TELEPHONE: (415) 576-0200  
42 (B) TELEFAX: (415) 576-0300  
43  
44  
45 (2) INFORMATION FOR SEQ ID NO:1:  
46

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47 (i) SEQUENCE CHARACTERISTICS:  
48 (A) LENGTH: 3 amino acids  
49 (B) TYPE: amino acid  
50 (C) STRANDEDNESS:  
51 (D) TOPOLOGY: linear  
52  
53 (ii) MOLECULE TYPE: peptide  
54  
55  
56 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
57  
58 Tyr Arg Gly  
59 1  
60  
61  
62 (2) INFORMATION FOR SEQ ID NO:2:  
63  
64 (i) SEQUENCE CHARACTERISTICS:  
65 (A) LENGTH: 4 amino acids  
66 (B) TYPE: amino acid  
67 (C) STRANDEDNESS:  
68 (D) TOPOLOGY: linear  
69  
70 (ii) MOLECULE TYPE: peptide  
71  
72  
73 (ix) FEATURE:  
74 (A) NAME/KEY: Modified-site  
75 (B) LOCATION: 3  
76 (D) OTHER INFORMATION: /product= "OTHER"  
77 /note= "Xaa = Ala or Ser"  
78  
79 (ix) FEATURE:  
80 (A) NAME/KEY: Modified-site  
81 (B) LOCATION: 4  
82 (D) OTHER INFORMATION: /product= "OTHER"  
83 /note= "Xaa = Arg or His"  
84  
85  
86 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
87  
88 Trp Glu Xaa Xaa  
89 1  
90  
91  
92 (2) INFORMATION FOR SEQ ID NO:3:  
93  
94 (i) SEQUENCE CHARACTERISTICS:  
95 (A) LENGTH: 1680 base pairs  
96 (B) TYPE: nucleic acid  
97 (C) STRANDEDNESS: single  
98 (D) TOPOLOGY: linear  
99

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100       (ii) MOLECULE TYPE: cDNA  
101  
102  
103       (ix) FEATURE:  
104           (A) NAME/KEY: -  
105           (B) LOCATION: 1..1680  
106           (D) OTHER INFORMATION: /note= "Arabidopsis APETALA2 (AP2)"  
107  
108  
109       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
110  
111 CTCTCTCTCT CTCTTTAGCT CTTTTTTTTT TTTTGTTC ATTAAAGTTT TTATTTATT       60  
112  
113 TTCTACCAAC CAAAAGCTTT TCTCTTGTT TTCTCTTATT TAGCTTCTAA CCTTGAGGAG       120  
114  
115 AATATACCAG AGGATTGAAG TTTAACCTT CAAAGATCAA AATCAAGAAA CCAAAAAAAA       180  
116  
117 ACAAAAAAAA TGTGGGATCT AAACGACGCA CCACACCAAA CACAAAGAGA AGAAGAATCT       240  
118  
119 GAAGAGTTTT GTTATTCTTC ACCAAGTAAA CGGGTTGGAT CTTTCTCTAA TTCAAGCTCT       300  
120  
121 TCAGCTGTTG TTATCGAAGA TGGATCCGAT GACGATGAAC TTAACCGGGT CAGACCCAAT       360  
122  
123 AACCCACTTG TCACCCATCA GTTCTCCCT GAGATGGATT CTAACGGCGG TGGTGTGCT       420  
124  
125 TCTGGCTTTC CTCGGGCTCA CTGGTTGGT GTTAAGTTTT GTCAGTCGGA TCTAGCCACC       480  
126  
127 GGATCGTCCG CGGGTAAAGC TACCAACGTT GCCGCTGCCG TAGTGGAGCC GGCACAGCCG       540  
128  
129 TTGAAAAAGA GTCGGCGTGG ACCAAGATCA AGAAGTTCTC AGTATAGAGG TGTTACGTTT       600  
130  
131 TACCGCGTA CCGGAAGATG GGAATCTCAT ATTTGGACT GTGGGAAACA AGTTTACTTA       660  
132  
133 GGTGGATTTG ACACTGCTCA TGCAGCAGCT CGAGCATATG ATAGAGCTGC TATTAAATTTC       720  
134  
135 CGTGGAGTAG AAGCGGATAT CAATTCAAC ATCGACGATT ATGATGATGA CTTGAAACAG       780  
136  
137 ATGACTAATT TAACCAAGGA AGAGTCGTA CACGTACTTC GCCGACAAAG CACAGGCTTC       840  
138  
139 CCTCGAGGAA GTTCGAAGTA TAGAGGTGTC ACTTTGCATA AGTGTGGTCG TTGGGAAGCT       900  
140  
141 CGTATGGTC AATTCTTAGG CAAAAAGTAT GTTTATTTGG GTTGTTCGA CACCGAGGTC       960  
142  
143 GAAGCTGCTA GAGCTTACGA TAAAGCTGCA ATCAAATGTA ACGGCAAAGA CGCCGTGACC       1020  
144  
145 AACTTTGATC CGAGTATTAA CGATGAGGAA CTCAATGCCG AGTCATCAGG GAATCCTACT       1080  
146  
147 ACTCCACAAG ATCACAACCT CGATCTGAGC TTGGGAAATT CGGCTAATTC GAAGCATAAA       1140  
148  
149 AGTCAAGATA TGCGGCTCAG GATGAACCAA CAACAACAAG ATTCTCTCCA CTCTAATGAA       1200  
150  
151 GTTCTTGGAT TAGGTCAAAC CGGAATGCTT AACCATACTC CCAATTCAAA CCACCAATTTC       1260  
152

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153	CCGGGCAGCA GCAACATTGG TAGCGGAGGC GGATTCTCAC TGTTTCCGGC GGCTGAGAAC	1320
154	CACCGGTTTG ATGGTCGGGC CTCGACGAAC CAAGTGTGA CAAATGCTGC AGCATCATCA	1380
155	GGATTCTCTC CTCATCATCA CAATCAGATT TTTAATTCTA CTTCTACTCC TCATCAAAAT	1440
156	TGGCTGCAGA CAAATGGCTT CCAACCTCCT CTCATGAGAC CTTCTTGAAT CTTTTATATT	1500
157	TTTAAGGTTT ATTATTATAT AAGAAAAACA AAAATGAACC TTTGAAATCC CCACATGTT	1560
158	TTGGTCATTT CATTAATCAT CGGCTTATAT TTTGCTTATT TTCCCCTAAA TCCTCTTGT	1620
159	AACTTAGGCG AACAAAAAAA ATTAATGGAA ATCTTTTCC CTCCATCGGT TACAAAAATA	1680
160		
161		
162		
163		
164		
165		
166		
167		
168	(2) INFORMATION FOR SEQ ID NO:4:	
169		
170	(i) SEQUENCE CHARACTERISTICS:	
171	(A) LENGTH: 67 amino acids	
172	(B) TYPE: amino acid	
173	(C) STRANDEDNESS:	
174	(D) TOPOLOGY: linear	
175		
176	(ii) MOLECULE TYPE: peptide	
177		
178		
179	(ix) FEATURE:	
180	(A) NAME/KEY: Peptide	
181	(B) LOCATION: 1..67	
182	(D) OTHER INFORMATION: /note= "AP2-R1 direct repeat at	
183	positions 129 to 195"	
184		
185	(ix) FEATURE:	
186	(A) NAME/KEY: Region	
187	(B) LOCATION: 32..49	
188	(D) OTHER INFORMATION: /note= "putative AP2-R1 amphipathic	
189	alpha-helix (SEQ ID NO:6)"	
190		
191		
192	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
193		
194	Ser Ser Gln Tyr Arg Gly Val Thr Phe Tyr Arg Arg Thr Gly Arg Trp	
195	1 5 10 15	
196		
197	Glu Ser His Ile Trp Asp Cys Gly Lys Gln Val Tyr Leu Gly Gly Phe	
198	20 25 30	
199		
200	Thr Asp Ala His Ala Ala Ala Arg Ala Tyr Asp Arg Ala Ala Ile Lys	
201	35 40 45	
202		
203	Phe Arg Gly Val Glu Ala Asp Ile Asn Phe Asn Ile Asp Asp Tyr Asp	
204	50 55 60	
205		

**RAW SEQUENCE LISTING  
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206 Asp Asp Leu  
207 65  
208  
209  
210 (2) INFORMATION FOR SEQ ID NO:5:  
211  
212 (i) SEQUENCE CHARACTERISTICS:  
213 (A) LENGTH: 68 amino acids  
214 (B) TYPE: amino acid  
215 (C) STRANDEDNESS:  
216 (D) TOPOLOGY: linear  
217  
218 (ii) MOLECULE TYPE: peptide  
219  
220  
221 (ix) FEATURE:  
222 (A) NAME/KEY: Peptide  
223 (B) LOCATION: 1..68  
224 (D) OTHER INFORMATION: /note= "AP2-R2 direct repeat at  
225 positions 221 to 288"  
226  
227 (ix) FEATURE:  
228 (A) NAME/KEY: Region  
229 (B) LOCATION: 33..50  
230 (D) OTHER INFORMATION: /note= "putative AP2-R2 amphipathic  
231 alpha-helix (SEQ ID NO:7)"  
232  
233  
234 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  
235  
236 Ser Ser Lys Tyr Arg Gly Val Thr Leu His Lys Cys Gly Arg Trp Glu  
237 1 5 10 15  
238  
239 Ala Arg Met Gly Gln Phe Leu Gly Lys Lys Tyr Val Tyr Leu Gly Leu  
240 20 25 30  
241  
242 Phe Asp Thr Glu Val Glu Ala Ala Arg Ala Tyr Asp Lys Ala Ala Ile  
243 35 40 45  
244  
245 Lys Cys Asn Gly Lys Asp Ala Val Thr Asn Phe Asp Pro Ser Ile Tyr  
246 50 55 60  
247  
248 Asp Glu Glu Leu  
249 65  
250  
251  
252 (2) INFORMATION FOR SEQ ID NO:6:  
253  
254 (i) SEQUENCE CHARACTERISTICS:  
255 (A) LENGTH: 18 amino acids  
256 (B) TYPE: amino acid  
257 (C) STRANDEDNESS:  
258 (D) TOPOLOGY: linear

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**SEQUENCE VERIFICATION REPORT  
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Original Text